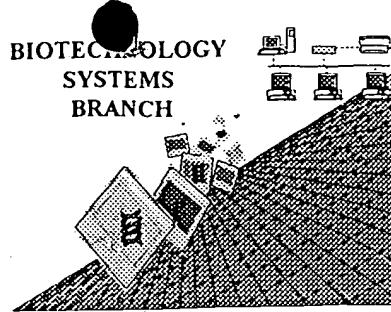


RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/781, 712 A

Source: 1635

Date Processed by STIC: 5-17-01

RECEIVED
JUN 04 2001
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/781,712 A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADER\$, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input checked="" type="checkbox"/> Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. <u>Valid response is Artificial Sequence.</u>	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

1635

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/781,712A

DATE: 05/17/2001
 TIME: 10:13:22

Input Set : A:\es.txt
 Output Set: N:\CRF3\05172001\I781712A.raw

Does Not Comply
 Corrected Diskette Needed
 See pp. 5-6

5 <110> APPLICANT: Crooke, Stanley T.
 6 Lima, Walter
 7 Wu, Hongjiang
 9 <120> TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
 12 <130> FILE REFERENCE: ISPH-0520
 14 <140> CURRENT APPLICATION NUMBER: US/09/781,712A
 15 <141> CURRENT FILING DATE: 2001-02-12
 17 <150> PRIOR APPLICATION NUMBER: US 09/684,254
 18 <151> PRIOR FILING DATE: 2000-10-06
 21 <150> PRIOR APPLICATION NUMBER: US 09/343,809
 22 <151> PRIOR FILING DATE: 1999-06-30
 25 <150> PRIOR APPLICATION NUMBER: US 09/203,716
 26 <151> PRIOR FILING DATE: 1998-12-02
 29 <150> PRIOR APPLICATION NUMBER: US 60/067,458
 30 <151> PRIOR FILING DATE: 1997-12-04
 33 <160> NUMBER OF SEQ ID NOS: 39
 36 <170> SOFTWARE: PatentIn version 3.0
 39 <210> SEQ ID NO: 1
 41 <211> LENGTH: 299
 43 <212> TYPE: PRT
 45 <213> ORGANISM: Homo sapiens
 49 <400> SEQUENCE: 1
 51 Met Asp Leu Ser Glu Leu Glu Arg Asp Asn Thr Gly Arg Cys Arg Leu
 52 1 5 10 15
 54 Ser Ser Pro Val Pro Ala Val Cys Arg Lys Glu Pro Cys Val Leu Gly
 55 20 25 30
 57 Val Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met Val Tyr Ala
 58 35 40 45
 60 Ile Cys Tyr Cys Pro Leu Pro Arg Leu Ala Asp Leu Glu Ala Leu Lys
 61 50 55 60
 63 Val Ala Asp Ser Lys Thr Leu Leu Glu Ser Glu Arg Glu Arg Leu Phe
 64 65 70 75 80
 66 Ala Lys Met Glu Asp Thr Asp Phe Val Gly Trp Ala Leu Asp Val Leu
 67 85 90 95
 69 Ser Pro Asn Leu Ile Ser Thr Ser Met Leu Gly Trp Val Lys Tyr Asn
 70 100 105 110
 72 Leu Asn Ser Leu Ser His Asp Thr Ala Thr Gly Leu Ile Gln Tyr Ala
 73 115 120 125
 75 Leu Asp Gln Gly Val Asn Val Thr Gln Val Phe Val Asp Thr Val Gly
 76 130 135 140
 78 Met Pro Glu Thr Tyr Gln Ala Arg Leu Gln Gln Ser Phe Pro Gly Ile
 79 145 150 155 160
 81 Glu Val Thr Val Lys Ala Lys Ala Asp Ala Leu Tyr Pro Val Val Ser
 82 165 170 175
 84 Ala Ala Ser Ile Cys Ala Lys Val Ala Arg Asp Gln Ala Val Lys Lys
 85 180 185 190
 87 Trp Gln Phe Val Glu Lys Leu Gln Asp Leu Asp Thr Asp Tyr Gly Ser

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/781,712A

DATE: 05/17/2001
TIME: 10:13:22

Input Set : A:\es.txt
Output Set: N:\CRF3\05172001\I781712A.raw

```

88      195          200          205
90 Gly Tyr Pro Asn Asp Pro Lys Thr Lys Ala Trp Leu Lys Glu His Val
91      210          215          220
93 Glu Pro Val Phe Gly Phe Pro Gln Phe Val Arg Phe Ser Trp Arg Thr
94 225          230          235          240
96 Ala Gln Thr Ile Leu Glu Lys Glu Ala Glu Asp Val Ile Trp Glu Asp
97          245          250          255
99 Ser Ala Ser Glu Asn Gln Glu Gly Leu Arg Lys Ile Thr Ser Tyr Phe
100         260          265          270
102 Leu Asn Glu Gly Ser Gln Ala Arg Pro Arg Ser Ser His Arg Tyr Phe
103         275          280          285
105 Leu Glu Arg Gly Leu Glu Ser Ala Thr Ser Leu
106         290          295
108 <210> SEQ ID NO: 2
110 <211> LENGTH: 128
112 <212> TYPE: PRT
114 <213> ORGANISM: Mus sp.
118 <400> SEQUENCE: 2
120 Met Asp Leu Ser Glu Leu Glu Arg Asp Asn Thr Gly Arg Cys Arg Leu
121 1          5          10          15
123 Ser Ser Pro Val Pro Ala Val Cys Leu Lys Glu Pro Cys Val Leu Gly
125          20          25          30
127 Val Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met Val Tyr Ala
128          35          40          45
130 Ile Cys Tyr Cys Pro Leu Ser Arg Leu Ala Asp Leu Glu Ala Leu Lys
131          50          55          60
133 Val Ala Asp Ser Lys Thr Leu Thr Glu Asn Glu Arg Glu Arg Leu Phe
134 65          70          75          80
136 Ala Lys Met Glu Glu Asp Gly Asp Phe Val Gly Trp Ala Leu Asp Val
137          85          90          95
139 Leu Ser Pro Asn Leu Ile Ser Thr Ser Met Leu Gly Arg Val Lys Tyr
140          100         105         110
142 Asn Leu Asn Ser Leu Ser His Asp Thr Ala Ala Gly Leu Ile Gln Tyr
143          115         120         125
145 <210> SEQ ID NO: 3
147 <211> LENGTH: 307
149 <212> TYPE: PRT
151 <213> ORGANISM: Caenorhabditis elegans
155 <400> SEQUENCE: 3
157 Ser Lys Thr Val Lys Tyr Phe Ile Glu Arg Met Ser Leu Lys Cys Glu
158 1          5          10          15
160 Thr Glu Arg Ser Lys Thr Trp Asn Asn Phe Gly Asn Gly Ile Pro Cys
161          20          25          30
163 Val Leu Gly Ile Asp Glu Ala Gly Arg Gly Pro Val Leu Gly Pro Met
164          35          40          45
166 Val Tyr Ala Ala Ala Ile Ser Pro Leu Asp Gln Asn Val Glu Leu Lys
167          50          55          60
169 Asn Leu Gly Val Asp Asp Ser Lys Ala Leu Asn Glu Ala Lys Arg Glu
170 65          70          75          80

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/781,712A

DATE: 05/17/2001
TIME: 10:13:22

Input Set : A:\es.txt
Output Set: N:\CRF3\05172001\I781712A.raw

172 Glu Ile Phe Asn Lys Met Asn Glu Asp Glu Asp Ile Gln Gln Ile Ile
173 85 90 95
175 Ala Tyr Ala Leu Arg Cys Leu Ser Pro Glu Leu Ile Ser Cys Ser Met
176 100 105 110
178 Leu Lys Arg Gln Lys Tyr Ser Leu Asn Glu Val Ser His Glu Ala Ala
179 115 120 125
181 Ile Thr Leu Ile Arg Asp Ala Leu Ala Cys Asn Val Asn Val Val Glu
182 130 135 140
184 Ile Lys Val Asp Thr Val Gly Pro Lys Ala Thr Tyr Gln Ala Lys Leu
185 145 150 155 160
187 Glu Lys Leu Phe Pro Gly Ile Ser Ile Cys Val Thr Glu Lys Ala Asp
188 165 170 175
190 Ser Leu Phe Pro Ile Val Ser Ala Ala Ser Ile Ala Ala Lys Val Thr
191 180 185 190
193 Arg Asp Ser Arg Leu Arg Asn Trp Gln Phe Arg Glu Lys Asn Ile Lys
194 195 200 205
196 Val Pro Asp Ala Gly Tyr Gly Ser Gly Tyr Pro Gly Asp Pro Asn Thr
197 210 215 220
199 Lys Lys Phe Leu Gln Leu Ser Val Glu Pro Val Phe Gly Phe Cys Ser
200 225 230 235 240
202 Leu Val Arg Ser Ser Trp Lys Thr Ala Ser Thr Ile Val Glu Lys Arg
203 245 250 255
205 Cys Val Pro Gly Ser Trp Glu Asp Asp Glu Glu Gly Lys Ser Gln
206 260 265 270
208 Ser Lys Arg Met Thr Ser Trp Met Val Pro Lys Asn Glu Thr Glu Val
209 275 280 285
211 Val Pro Lys Arg Asn Met Glu Ile Asn Leu Thr Lys Ile Val Ser Thr
212 290 295 300
214 Leu Phe Leu
215 305
217 <210> SEQ ID NO: 4
219 <211> LENGTH: 307
221 <212> TYPE: PRT
223 <213> ORGANISM: Saccharomyces cerevisiae
227 <400> SEQUENCE: 4
229 Met Val Pro Pro Thr Val Glu Ala Ser Leu Glu Ser Pro Tyr Thr Lys
230 1 5 10 15
232 Ser Tyr Phe Ser Pro Val Pro Ser Ala Leu Leu Glu Gln Asn Asp Ser
233 20 25 30
235 Pro Ile Ile Met Gly Ile Asp Glu Ala Gly Arg Gly Pro Val Leu Gly
236 35 40 45
238 Pro Met Val Tyr Ala Val Ala Tyr Ser Thr Gln Lys Tyr Gln Asp Glu
239 50 55 60
241 Thr Ile Ile Pro Asn Tyr Glu Phe Asp Asp Ser Lys Lys Leu Thr Asp
242 65 70 75 80
244 Pro Ile Arg Arg Met Leu Phe Ser Lys Ile Tyr Gln Asp Asn Glu Glu
245 85 90 95
247 Leu Thr Gln Ile Gly Tyr Ala Thr Thr Cys Ile Thr Pro Leu Asp Ile
249 100 105 110

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/781,712A

DATE: 05/17/2001
TIME: 10:13:22

Input Set : A:\es.txt
Output Set: N:\CRF3\05172001\I781712A.raw

251 Ser Arg Gly Met Ser Lys Phe Pro Pro Thr Arg Asn Tyr Asn Leu Asn
252 115 120 125
254 Glu Gln Ala His Asp Val Thr Met Ala Leu Ile Asp Gly Val Ile Lys
255 130 135 140
257 Gln Asn Val Lys Leu Ser His Val Tyr Val Asp Thr Val Gly Pro Pro
258 145 150 155 160
260 Ala Ser Tyr Gln Lys Lys Leu Glu Gln Arg Phe Pro Gly Val Lys Phe
261 165 170 175
263 Thr Val Ala Lys Lys Ala Asp Ser Leu Tyr Cys Met Val Ser Val Ala
264 180 185 190
266 Ser Val Val Ala Lys Val Thr Arg Asp Ile Leu Val Glu Ser Leu Lys
267 195 200 205
269 Arg Asp Pro Asp Glu Ile Leu Gly Ser Gly Tyr Pro Ser Asp Pro Lys
270 210 215 220
272 Thr Val Ala Trp Leu Lys Arg Asn Gln Thr Ser Leu Met Gly Trp Pro
273 225 230 235 240
275 Ala Asn Met Val Arg Phe Ser Trp Gln Thr Cys Gln Thr Leu Leu Asp
276 245 250 255
278 Asp Ala Ser Lys Asn Ser Ile Pro Ile Lys Trp Glu Glu Gln Tyr Met
279 260 265 270
281 Asp Ser Arg Lys Asn Ala Ala Gln Lys Thr Lys Gln Leu Gln Leu Gln
282 275 280 285
284 Met Val Ala Lys Pro Val Arg Arg Lys Arg Leu Arg Thr Leu Asp Asn
285 290 295 300
287 Trp Tyr Arg
288 305
290 <210> SEQ ID NO: 5
292 <211> LENGTH: 198
294 <212> TYPE: PRT
296 <213> ORGANISM: Escherichia coli
300 <400> SEQUENCE: 5
302 Met Ile Glu Phe Val Tyr Pro His Thr Gln Leu Val Ala Gly Val Asp
303 1 5 10 15
305 Glu Val Gly Arg Gly Pro Leu Val Gly Ala Val Val Thr Ala Ala Val
306 20 25 30
308 Ile Leu Asp Pro Ala Arg Pro Ile Ala Gly Leu Asn Asp Ser Lys Lys
309 35 40 45
311 Leu Ser Glu Lys Arg Arg Leu Ala Leu Tyr Glu Glu Ile Lys Glu Lys
312 50 55 60
314 Ala Leu Ser Trp Ser Leu Gly Arg Ala Glu Pro His Glu Ile Asp Glu
315 65 70 75 80
317 Leu Asn Ile Leu His Ala Thr Met Leu Ala Met Gln Arg Ala Val Ala
318 85 90 95
320 Gly Leu His Ile Ala Pro Glu Tyr Val Leu Ile Asp Gly Asn Arg Cys
321 100 105 110
323 Pro Lys Leu Pro Met Pro Ala Met Ala Val Val Lys Gly Asp Ser Arg
324 115 120 125
326 Val Pro Glu Ile Ser Ala Ala Ser Ile Leu Ala Lys Val Thr Arg Asp
327 130 135 140

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/781,712A

DATE: 05/17/2001
TIME: 10:13:22

Input Set : A:\es.txt
Output Set: N:\CRF3\05172001\I781712A.raw

329 Ala Glu Met Ala Ala Leu Asp Ile Val Phe Pro Gln Tyr Gly Phe Ala
 330 145 150 155 160
 332 Gln His Lys Gly Tyr Pro Thr Ala Phe His Leu Glu Lys Leu Ala Glu
 333 165 170 175
 335 His Gly Ala Thr Glu His His Arg Arg Ser Phe Gly Pro Val Lys Arg
 336 180 185 190
 338 Ala Leu Gly Leu Ala Ser
 339 195
 341 <210> SEQ ID NO: 6
 343 <211> LENGTH: 286
 345 <212> TYPE: PRT
 347 <213> ORGANISM: Homo sapiens
 351 <300> PUBLICATION INFORMATION:
 353 <302> TITLE: Human Type 2 RNase H
 W--> 355 <309> DATABASE ENTRY DATE: → Do not enter <309> if you do
 W--> 357 <310> PATENT DOC NO: US/09/203,726 not have a <308> Database Accession
 359 <311> PATENT FILING DATE: 1998-12-02
 361 <312> PUBLICATION DATE: 1999-12-14
 365 <400> SEQUENCE: 6
 367 Met Ser Trp Leu Leu Phe Leu Ala His Arg Val Ala Leu Ala Leu
 368 1 5 10 15
 370 Pro Cys Arg Arg Gly Ser Arg Gly Phe Gly Met Phe Tyr Ala Val Arg
 371 20 25 30
 373 Arg Gly Arg Lys Thr Gly Val Phe Leu Thr Trp Asn Glu Cys Arg Ala
 374 35 40 45
 376 Gln Val Asp Arg Phe Pro Ala Ala Arg Phe Lys Lys Phe Ala Thr Glu
 377 50 55 60
 379 Asp Glu Ala Trp Ala Phe Val Arg Lys Ser Ala Ser Pro Glu Val Ser
 380 65 70 75 80
 382 Glu Gly His Glu Asn Gln His Gly Gln Glu Ser Glu Ala Lys Pro Gly
 383 85 90 95
 385 Lys Arg Leu Arg Glu Pro Leu Asp Gly Asp Gly His Glu Ser Ala Gln
 386 100 105 110
 388 Pro Tyr Ala Lys His Met Lys Pro Ser Val Glu Pro Ala Pro Pro Val
 389 115 120 125
 391 Ser Arg Asp Thr Phe Ser Tyr Met Gly Asp Phe Val Val Val Tyr Thr
 392 130 135 140
 394 Asp Gly Cys Cys Ser Ser Asn Gly Arg Arg Lys Pro Arg Ala Gly Ile
 395 145 150 155 160
 397 Gly Val Tyr Trp Gly Pro Gly His Pro Leu Asn Val Gly Ile Arg Leu
 398 165 170 175
 400 Pro Gly Arg Gln Thr Asn Gln Arg Ala Glu Ile His Ala Ala Cys Lys
 401 180 185 190
 403 Ala Ile Glu Gln Ala Lys Thr Gln Asn Ile Asn Lys Leu Val Leu Tyr
 404 195 200 205
 406 Thr Asp Ser Met Phe Thr Ile Asn Gly Ile Thr Asn Trp Val Gln Gly
 407 210 215 220
 409 Trp Lys Lys Asn Gly Trp Lys Thr Ser Ala Gly Lys Glu Val Ile Asn
 410 225 230 235 240

09/781, 712 A

p. 6

<210> 13 Seg. #13

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Sense primer

<400> 13

agcaggcgcc gcttcgaggg

20

<210> 14 Seg #14

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Sense primer

<400> 14

cccgctcctg cagtattagt tcttgc

<210> 15 Seg #15

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Sense primer

<400> 15

ttgcagctgg tgggtggcggc tgagg

25

Circled <213> responses
are incomplete as per section
1.823b of the new sequence
rules. See #11 on the Error
Summary Sheet.

Note: This error occurs
²⁶ throughout the sequence listing.
please review and correct.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/781,712A

DATE: 05/17/2001
TIME: 10:13:23

Input Set : A:\es.txt
Output Set: N:\CRF3\05172001\I781712A.raw

L:355 M:286 W: Invalid Database Entry: Valid Formats YYYY-MM-DD or Mon-YYYY, SEQ ID:6
L:357 M:284 W: Blank Line not Allowed, <310> field identifier
L:908 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:926 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:945 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:963 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:981 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:999 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:1017 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:1035 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:1053 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:1071 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:1089 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:1107 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:1126 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:1144 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:1162 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:1181 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:1199 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:1217 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:1235 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:1253 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:1271 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:1289 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:1307 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:1325 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:1343 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:1361 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:1379 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39